Listing of claims:

This listing of claims will replace all prior versions and listings of claims in the application. Please amend the application by amending claims 1, 3, 9-10, 18, 20, 25-26, 34-35, and 37-38; canceling claims 8, 24, and 36; and adding new claims 43-61 as indicated below.

1. (Currently Amended) A method for identifying oligonucleotide sequences suitable for the amplification of a unique sequence within a genomic region of interest, said method comprising the steps of:

executing a first process on a digital computer to identify repeat sequences that occur within said genomic region of interest;

executing a second process on a digital computer to compare repeat sequence-free subsequences within said genomic region of interest to a nucleotide sequence database, whereby nucleotide sequences within said nucleotide sequence database that are ~~substantially similar~~ at least 50% identical to said repeat sequence-free subsequences are identified;

executing a third process on a digital computer to identify oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within at least one of said repeat sequence-free subsequences for which ~~a defined number of~~ 5 or fewer ~~substantially similar~~ sequences that are at least 50% identical are identified in said nucleotide sequence database; and

outputting said oligonucleotide sequences.

2. (Original) The method of claim 1, wherein said genomic region is from a human genome.

3. (Currently Amended) The method of claim 1, wherein ~~said defined number of substantially similar sequences is zero~~ the third process comprises identifying oligonucleotide sequences that are suitable for use as primers in an amplification reaction

to amplify a product within at least one of said repeat sequence-free subsequences that lacks any sequences that are at least 50% identical to said nucleotide sequence database.

4. (Original) The method of claim 1, wherein said oligonucleotide sequences are outputted by displaying the sequences on a computer screen or on a computer printout.

5. (Original) The method of claim 1, wherein said oligonucleotide sequences are outputted by executing a fourth process on a digital computer to direct the synthesis of oligonucleotide primers comprising said oligonucleotide sequences.

6. (Original) The method of claim 5, wherein said computer directs the synthesis of said oligonucleotide primers by ordering said synthesis from an external source.

7. (Original) The method of claim 5, wherein said computer is in communication with an oligonucleotide synthesizer, and wherein said computer directs the synthesis of said oligonucleotide primers by said synthesizer.

8. (Canceled)

9. (Currently Amended) The method of claim 1, wherein said 5 or fewer ~~substantially similar~~ sequences are at least ~~about~~ 70% identical to said repeat sequence-free subsequences.

10. (Currently Amended) The method of claim 1, wherein said 5 or fewer ~~substantially similar~~ sequences are at least ~~about~~ 90% identical to said repeat sequence-free subsequences.

11. (Previously Amended) The method of claim 1, wherein said first process is executed using a software program that screens sequences for:

i. interspersed repeats that are known to exist in mammalian genomes and;

ii. low complexity DNA sequences.

12. (Previously Amended) The method of claim 1, wherein said second process is executed using a sequence comparison algorithm.

13. (Original) The method of claim 1, wherein said third process is executed using Primer3 software.

14. (Original) The method of claim 5, further comprising producing an amplification product using said oligonucleotide primers.

15. (Original) The method of claim 14, wherein said amplification product is a FISH probe.

16. (Original) The method of claim 15, wherein said FISH probe is fluorescently labeled.

17. (Original) The method of claim 14, wherein said amplification product is an array CGH target.

18. (Currently Amended) A method for identifying oligonucleotide sequences suitable for the amplification of a unique sequence within a genomic region of interest, said method comprising the steps of:

analyzing a genomic nucleotide sequence that encompasses said genomic region of interest to identify repeat sequences within said genomic region;

comparing at least one repeat sequence-free subsequence within said genomic nucleotide sequence to a nucleotide sequence database to identify sequences within said database that are ~~substantially similar~~ at least 50% identical to said repeat sequence-free subsequence;

for at least one of said repeat sequence-free subsequences for which ~~a defined number of~~ 5 or fewer ~~substantially similar~~ sequences that are at least 50% identical are identified within said nucleotide sequence database, selecting oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within said repeat sequence-free subsequence.

19. (Original) The method of claim 18, wherein said genomic region is from a human genome.

20. (Currently Amended) The method of claim 18, wherein said ~~defined number of substantially similar sequences is zero~~ oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within said repeat sequence-free subsequence are selected from at least one of said repeat sequence-free subsequences that lack any sequences that are at least 50% identical to said nucleotide sequence database.

21. (Original) The method of claim 18, further comprising displaying said oligonucleotide sequences on a computer screen or on a computer printout.

22. (Original) The method of claim 18, further comprising directing the synthesis of oligonucleotide primers comprising said oligonucleotide sequences.

23. (Original) The method of claim 22, wherein said synthesis is directed by ordering the synthesis of said primers from an external source.

24. (Canceled)

25. (Currently Amended) The method of claim 18, wherein said 5 or fewer ~~substantially similar~~ sequences are at least ~~about~~ 70% identical to said repeat sequence-free subsequences.

26. (Currently Amended) The method of claim 18, wherein said 5 or fewer ~~substantially similar~~ sequences are at least ~~about~~ 90% identical to said repeat sequence-free subsequences.

27. (Previously Amended) The method of claim 18, wherein the identification of repeat sequences within said genomic region is performed using a software program that screens sequences for:

i. interspersed repeats that are known to exist in mammalian genomes and;

ii. low complexity DNA sequences.

28. (Previously Amended) The method of claim 18, wherein the comparison of said at least one repeat sequence-free subsequence with said genome database is performed using a sequence comparison algorithm.

29. (Original) The method of claim 18, wherein said oligonucleotide sequences are selected using Primer3 software.

30. (Original) The method of claim 22, further comprising generating an amplification product using said oligonucleotide primers.

31. (Original) The method of claim 30, wherein said amplification product is a FISH probe.

32. (Original) The method of claim 31, wherein said FISH probe is fluorescently labeled.

33. (Original) The method of claim 30, wherein said amplification product is an array CGH target.

34. (Currently Amended) A computer program product designing and outputting oligonucleotide sequences suitable for use as primers to amplify unique sequences within a genomic region of interest, said computer program product comprising:

a storage structure having computer program code embodied therein, said computer program code comprising:

computer program code for causing a computer to analyze a nucleotide sequence encompassing said genomic region of interest to identify repeat sequences within said nucleotide sequence;

computer program code for causing a computer to, for each subsequence of said nucleotide sequence that does not contain any of said repeat sequences, compare

said subsequence against a nucleotide sequence database to identify nucleotide sequences within said database that are ~~substantially similar~~ at least 50% identical to said subsequence;

computer program code for causing a computer to, for ~~each~~ at least one of said subsequences for which ~~a defined number of~~ 5 or fewer ~~substantially similar~~ sequences that are at least 50% identical are found in said database, identify oligonucleotide sequences suitable for use as primers in an amplification reaction to amplify a product within said subsequence; and

computer program code for outputting said oligonucleotide sequences.

35. (Currently Amended) The method of claim 34, wherein said ~~defined number of substantially similar sequences is zero~~ oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within said subsequence are identified from at least one of said subsequences that lack any sequences that are at least 50% identical to said database.

36. (Canceled)

37. (Currently Amended) The method of claim 34, wherein said 5 or fewer ~~substantially similar~~ sequences are at least ~~about~~ 70% identical to said subsequences.

38. (Currently Amended) The method of claim 34, wherein said 5 or fewer ~~substantially similar~~ sequences are at least ~~about~~ 90% identical to said subsequences.

39. (Canceled)

40. (Previously Added) The method of claim 1, wherein the repeat-free subsequences are each at least 100 bp long.

41. (Previously Added) The method of claim 18, wherein the repeat-free subsequences are each at least 100 bp long.

42. (Previously Added) The computer program of claim 34, wherein each nucleotide sequence that does not contain any of the repeat sequences is at least 100 bp long.

43. (New) A method for identifying oligonucleotide sequences suitable for the amplification of a unique sequence within a genomic region of interest, said method comprising the steps of:

executing a first process on a digital computer to identify repeat sequences that occur within said genomic region of interest;

executing a second process on a digital computer to compare repeat sequence-free subsequences within said genomic region of interest to a nucleotide sequence database, whereby at least one repeat sequence-free subsequences that is at least 90% identical to a nucleotide sequence within said nucleotide sequence database is discarded;

executing a third process on a digital computer to identify oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within at least one repeat sequence-free subsequences remaining after executing said second process; and

outputting said oligonucleotide sequences.

44. (New) The method of claim 43, wherein said genomic region is from a human genome.

45. (New) The method of claim 43, wherein said oligonucleotide sequences are outputted by displaying the sequences on a computer screen or on a computer printout.

46. (New) The method of claim 43, wherein said oligonucleotide sequences are outputted by executing a fourth process on a digital computer to direct the synthesis of oligonucleotide primers comprising said oligonucleotide sequences.

47. (New) The method of claim 43, wherein said computer directs the synthesis of said oligonucleotide primers by ordering said synthesis from an external source.

48. (New) The method of claim 43, wherein said computer is in communication with an oligonucleotide synthesizer, and wherein said computer directs the synthesis of said oligonucleotide primers by said synthesizer.

49. (New) The method of claim 43, wherein all repeat sequence-free subsequences that are at least 70% identical to a nucleotide sequence within said nucleotide sequence database are discarded.

50. (New) The method of claim 43, wherein all repeat sequence-free subsequences that are at least 50% identical to a nucleotide sequence within said nucleotide sequence database are discarded.

51. (New) The method of claim 43, wherein said first process is executed using a software program that screens sequences for:

i. interspersed repeats that are known to exist in mammalian genomes and;

ii. low complexity DNA sequences.

52. (New) The method of claim 43, wherein said second process is executed using a sequence comparison algorithm.

53. (New) The method of claim 43, wherein said third process is executed using Primer3 software.

54. (New) The method of claim 43, further comprising producing an amplification product using said oligonucleotide primers.

55. (New) The method of claim 43, wherein said amplification product is a FISH probe.

56. (New) The method of claim 43, wherein said FISH probe is fluorescently labeled.

57. (New) The method of claim 43, wherein said amplification product is an array CGH target.

58. (New) The method of claim 43, wherein the repeat-free subsequences are each at least 100 bp long.

59. (New) The method of claim 43, wherein all repeat sequence-free subsequences that are at least 90% identical to a nucleotide sequence within said nucleotide sequence database are discarded.

60. (New) A method for identifying oligonucleotide sequences suitable for the amplification of a unique sequence within a genomic region of interest, said method comprising the steps of:

(1) analyzing a genomic nucleotide sequence that encompasses said genomic region of interest to identify repeat sequences within said genomic region;

(2) comparing repeat sequence-free subsequences within said genomic region of interest to a nucleotide sequence database, whereby at least one repeat sequence-free subsequences that is at least 90% identical to a nucleotide sequence within said nucleotide sequence database is discarded;

(3) identifying oligonucleotide sequences that are suitable for use as primers in an amplification reaction to amplify a product within at least one repeat sequence-free subsequences remaining after step (2).

61. (New) A computer program product designing and outputting oligonucleotide sequences suitable for use as primers to amplify unique sequences within a genomic region of interest, said computer program product comprising a storage structure having computer program code embodied therein, said computer program code comprising the elements:

(1) computer program code for causing a computer to analyze a nucleotide sequence encompassing said genomic region of interest to identify repeat sequences within said nucleotide sequence;